

Please amend claim 32.

In the claims

1-31. (canceled)

32. (currently amended) A method comprising steps of:

providing a DNA polymerase having an amino acid sequence that shows at least 30% overall identity with that of the polypeptide encoded by SEQ ID NO:4, and further includes a 15 amino-acid motif that is identical to one of SEQ ID NOs 5-22 ~~except that it~~ or contains up to 3 amino acid substitutions as compared with the one of SEQ ID NO 5-22; the polymerase having an enhanced ability to incorporate a dye-labelled acyclonucleotide compared with a dye-labelled dideoxy nucleotide into a single strand DNA when determined by an assay utilizing a primed single strand DNA and a fixed concentration of dNTPs and increasing amounts of the dye-labelled acyclonucleotide or dye-labelled dideoxy nucleotide and analyzing the labeled product ;

contacting the DNA polymerase with a template, a primer that binds to the template, and a collection of nucleotides including at least one acyclonucleotide; and

incubating the DNA polymerase with the template and the nucleotides so that the DNA polymerase extends the primer by incorporating the nucleotides .

33. (previously presented) The method of claim 32, wherein the DNA polymerase has an amino acid sequence that shows at least 70% overall identity with that of SEQ ID NO:4.

34. (previously presented) The method of claim 32 or claim 33, wherein the 15 amino-acid motif is identical to one of SEQ ID NOs 5-22.

35. (previously presented) The method of claim 32 or claim 33, wherein the 15 amino-acid motif is identical to one of SEQ ID NOs 5-17 except that it contains up to 3 amino acid substitutions as compared with the SEQ ID NO.

36. (previously presented) The method of claim 35, wherein the 15 amino acid motif is identical to one of SEQ ID NOs 5-17.

37. (previously presented) The method of claim 32 or 33, wherein the 15 amino acid motif is identical to one of SEQ ID NOs 5-8 except that it contains up to 3 amino acid substitutions as compared with the SEQ ID NO.

38. (previously presented) The method of claim 37, wherein the 15 amino acid motif is identical to one of SEQ ID NOs 5-8.

39. (previously presented) The method of claim 32 or 33, wherein the step of incubating comprises incubating the DNA polymerase with the template and the nucleotides so that the DNA polymerase extends the primer by

incorporating the nucleotides, and preferentially incorporates acyclonucleotides.

40. (previously presented) The method of claim 32 or 33, wherein the 15 amino acid motif has up to one amino acid substitution as compared with one of SEQ ID NOs 5-22.

41. (previously presented) The method of claim 35, wherein the 15 amino acid motif has up to one amino acid substitution as compared with one of SEQ ID NOs 5-17.

42. (previously presented) The method of claim 37, wherein the 15 amino acid motif has up to one amino acid substitution as compared with one of SEQ ID NOs 5-8.

43. (previously presented) The method of claim 32 or 33 wherein the DNA polymerase is VentEM, Deep Vent™, 90 N, *Pfii*, VentT'/488L, or 90N/485L.